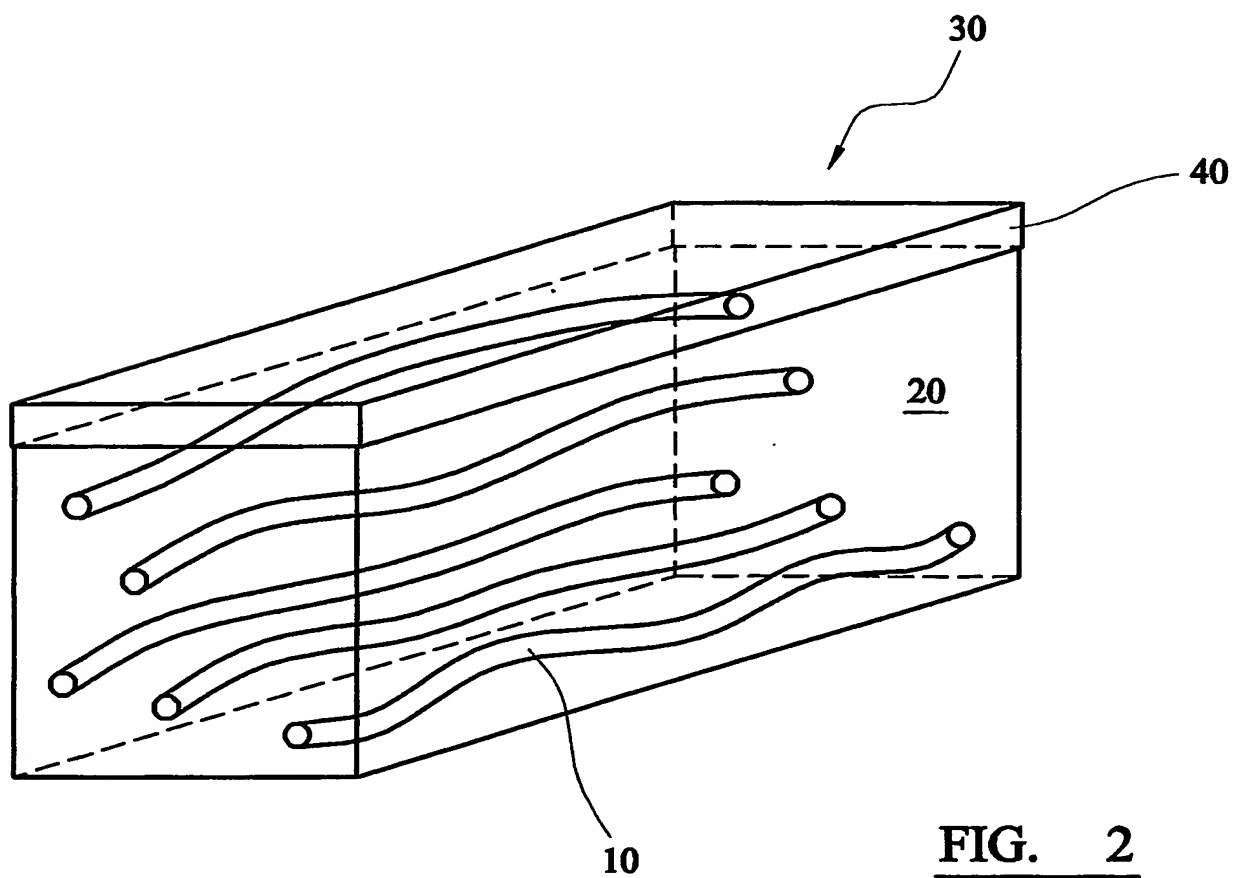
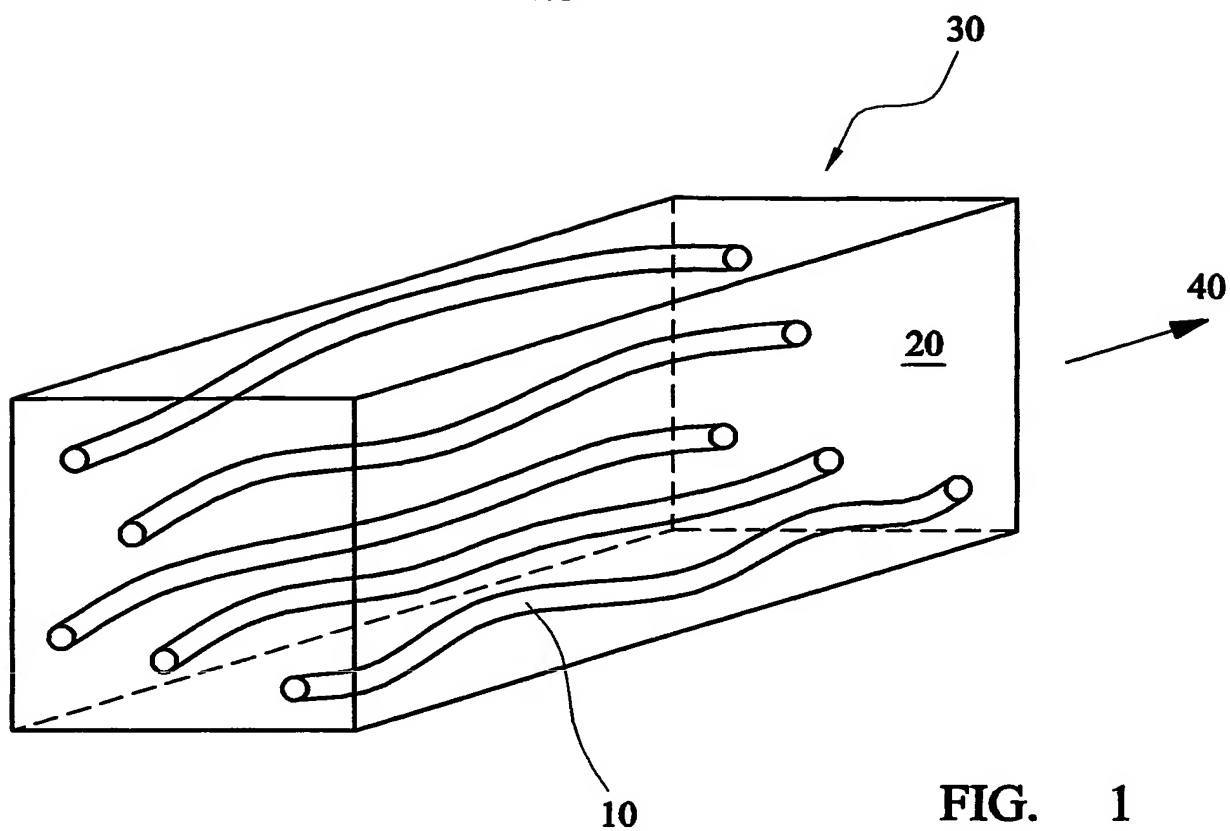


-1/5-



-2/5-

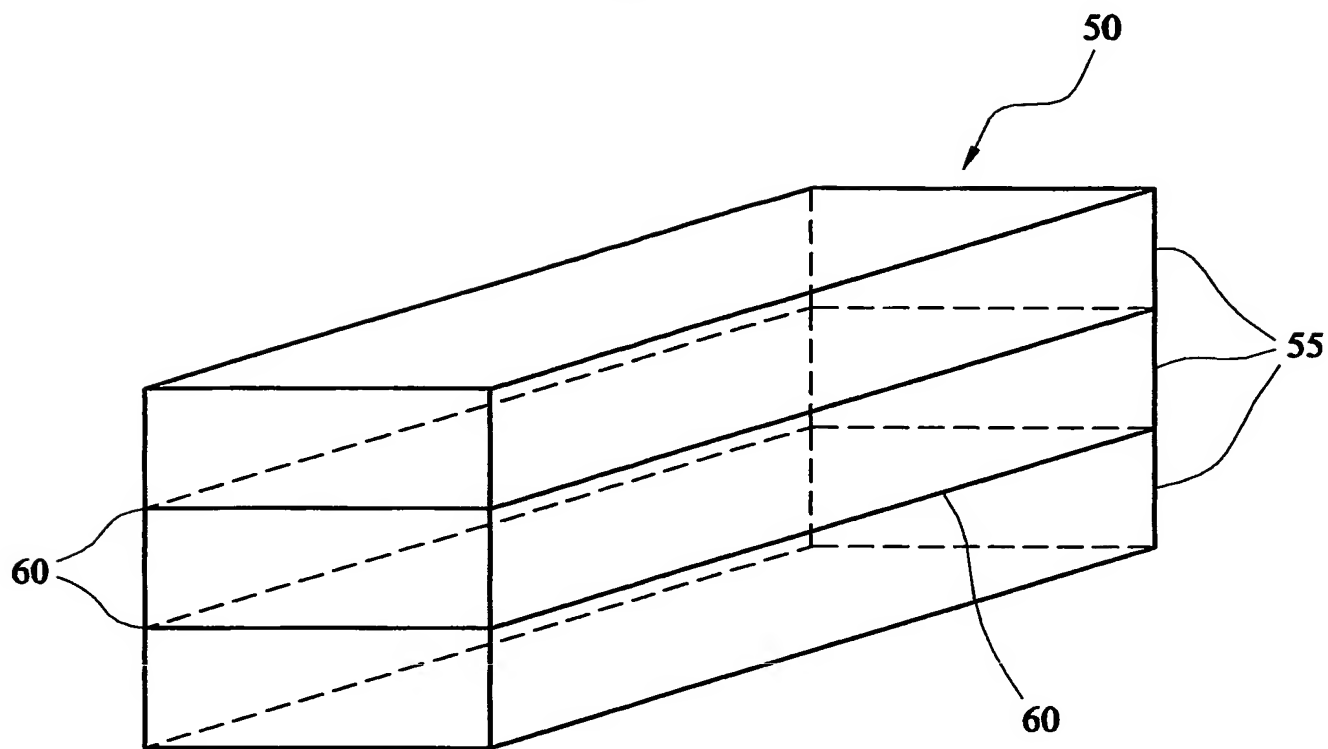


FIG. 3

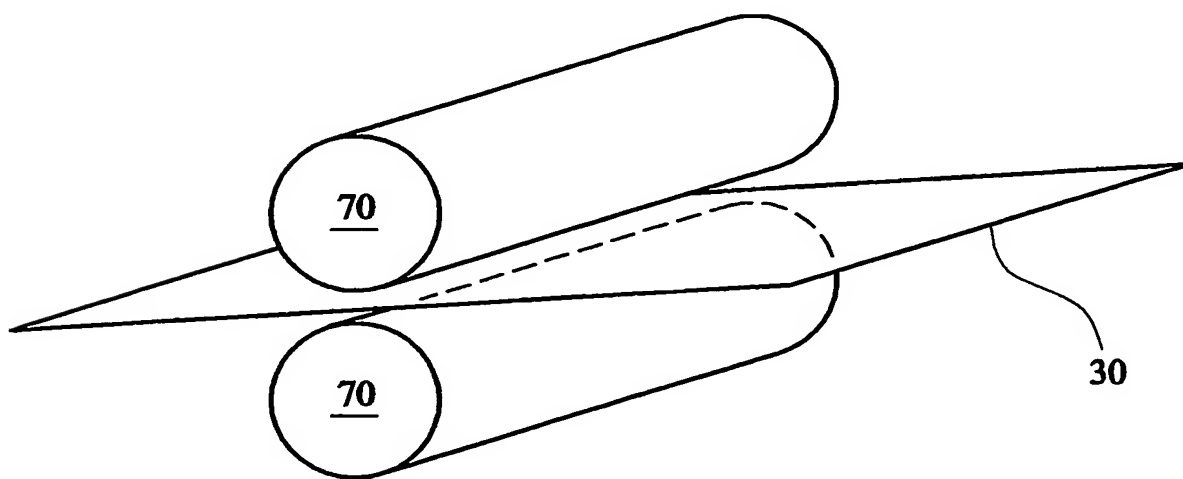


FIG. 4

-3/5-

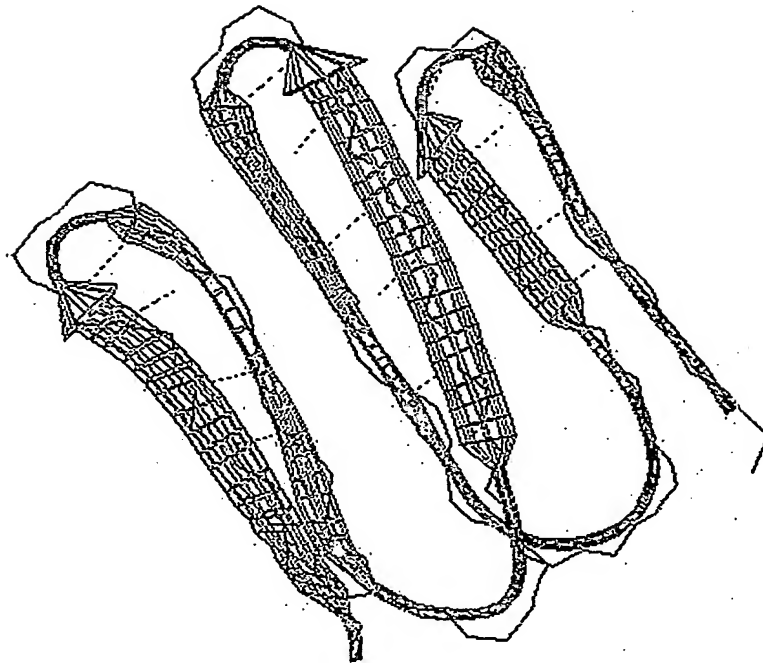
Consensus repeat structure of sericin precursor protein

No. of Repeats	Total Score	Length	Diagonal	BW-From	BW-To	Level
7	529.97	35	35	317	351	1

131-	164	(46.31/ 7.35)	SSSSSTeeSS...SSSR..AASSTDASSNTDSNSNSA
165-	202	(82.44/20.60)	GSSTSGG..RRTYGYSSNSRDGSVSTGSSSENTDSNSGNA
203-	240	(83.27/20.91)	GSSTSGG..SSTYGYSSNSRDGSVSTTGSSSENTDSNSNSV
241-	278	(68.12/15.35)	GSRRSGG..SSSHEDSSKSRDENVBTTGSSSENTDSNSNSV
279-	316	(82.44/20.60)	GSSTSGG..RRTYGYSSNSRDGSVSTGSSSENTDSNSNSV
317-	354	(84.15/21.23)	GSSTSGG..SSTYGYSSNSRDGSVSTGSSSENTDSNSNSA
355-	389	(83.23/20.90)	GSSTSGG..SSTYGYSSNSHDSVSTGSSSENTDSNS

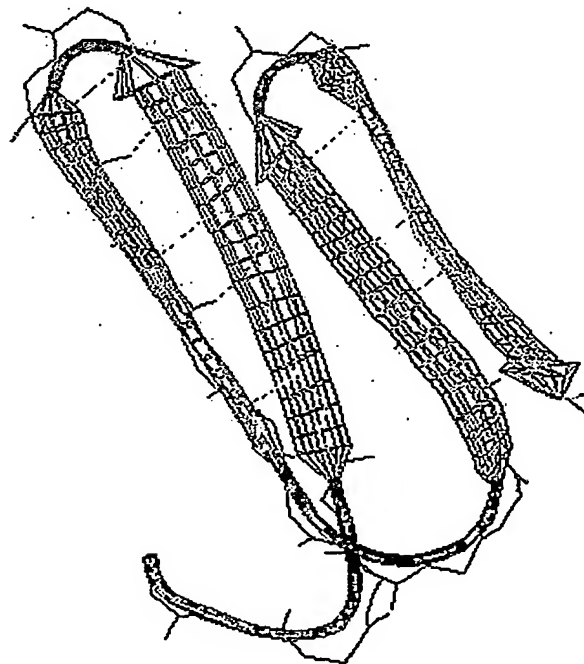
FIG. 5

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Ice nucleation protien (inaz) from the published PDB file

FIG. 6



**Swiss model for consensus sequence of sericin precursor protein using
inaz as a template**

FIG. 7

	500	510	520	530	540	550
INAZ	STGTAGADSSLIAGYGSTQTSGSESSLTAGYGSTQTAREGSTLTAGYGSTGTAGADSSLI					
	:. . .	: :	. :	::: .	:::
serici	SAGAHRAKSVEQSQDKSKYTTSGPEGVSTSGRSQNYKDSKQAIISGGTKSSNSNVQSDEKS					
	60	70	80	90	100	110
	560	570	580	590	600	610
INAZ	AGYGSTQTSGSESSLTAGYGSTQTAQQGSVLTSGYGSTQTAGAASNLTGYGSTGTAGHB					
	:	:.
serici	ASQSSSRSSQESASYSSSSSSSTEESSSSSSRAASSTDASSNTDSNSNSAGSSTSGGRR					
	120	130	140	150	160	170
	620	630	640	650	660	670
INAZ	SFIIAGY---GSTQTAGHKSILTAGYGSTQTARDGSDLIAGYGSTGTAGS---GSSLIA					
	:	: :	:
serici	TYGYSSNSRDGVSSTTGSSSNTDSNSSNAGSSTSGGSSTYGYSSNSRDGVSSTTGSSSNT					
	180	190	200	210	220	230
	680	690	700	710	720	730
INAZ	GYGSTQTASYRSMLTAGYGSTQTAREHSDLVTGYGSTSTAGSNSSLIAGYGSTQTAGFKS					
	:	: :	:	:	:
serici	DSNSNSVSGRRSGGSSSHEDSSKSRDENVTGSSSNTDSNSNSVGSSTSGGRRTYGYSS					
	240	250	260	270	280	290

SUBSTITUTE SHEET (RULE 26)